



097702887760

	1				50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAS
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA</u>	<u>SATV-TAVLA</u>	<u>TLL-ATVQA-</u>

C1

	51				100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.VTED	SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRVTA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
H38	ATDED...EEE	ELEPVVRSAL	VLQFMIDKEG	NGENE.STGN	IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSAL	VLQFMIDKEG	NGEIESTGDI	GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SGELET...I	SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SVELET...I	SLSMTNDSKE
Consensus	-----	-L--V-R---	V-----EG	--E-E-----	-----

V1

	101				150
EG327	GVLTAGTITL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSSFTYSLK	KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK	KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK	KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNNTNENT	NDSSFTYSLK	KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD.....FTYSLK	KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTGILNVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK	KDLTGILNVE
Consensus	-----TL	<u>KAGDNLKIKQ</u>	-----	----FTYSLK	<u>K-L--L--V-</u>

V1

C2

V2

C3

FIG. 1

	151				200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE	TNGDPTVHLN	GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDM
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNI-SDTK</u>	<u>GLNFAK-TA-</u>	<u>TNGD-TVHLN</u>	<u>GIGSTLTD-L</u>

C3

	201				250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVP	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVP	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
Consensus	<u>----A-----</u>	<u>----T-----</u>	<u>RAAS-KDVLN</u>	<u>AGWNIKGVP</u>	<u>G-T-----NV</u>

V3

C4

V4

	251				300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
H38	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGKL
Consensus	<u>DFV-TYDTVE</u>	<u>FLSADTKTTT</u>	<u>VNVESKDNGK</u>	<u>-TEVKIGAKT</u>	<u>SVIKEKDGKL</u>

C5

FIG. 1

	301		350
EG327	VTGKDKGEND	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ198	VTGKGKDENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ10	VTGKGKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H15	VTGKGKDENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
EG329	VTGKDKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
PMC21	VTGKDKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H38	VTGKGKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
P20	VTGKGKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Z2491	VTGKGKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H41	VTGKGKGENG	SSTDKEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN KAGWRMKTTT ANGQTGQADK</u>

C5

	351		400
EG327	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTS GTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
H15	FETVTS GTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
EG329	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H38	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
P20	FETVTS GTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTS GTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H41	FETVTS GTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Consensus	<u>FETVTS GT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGNI TV-YDVNVGD ALNVNQLQNS</u>

C5

	401		450
EG327	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ10	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H15	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H38	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
P20	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EISRNGKNID
H41	GWNLD SKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus	<u>GWNLD SKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>

C5

FIG. 1

451 500

EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

501 550

EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

551 600

EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

FIG. 1

5/31

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	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

FIG. 1

	1						70
H15	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ10	ATGAACAAAA	TATCCCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
BZ198	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
P20	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	AGTCGTATCC	GAGCTCACAC
H38	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Z2491	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
H41	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
EG329	ATGAACGAAA	TATTGCGCAT	CATTTGGAAT	AGCGCCCTCA	ATGCCTGGGT	CGTTGTATCC	GAGCTCACAC
PMC21	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC
EG327	ATGAACAAAA	TATACCGCAT	CATTTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Consensus	<u>ATGAAC-AAA</u>	<u>TAT--CGCAT</u>	<u>CATTTGGAAT</u>	<u>AG-GCCCTCA</u>	<u>ATGC-TGGGT</u>	<u>-G--GTATCC</u>	<u>GAGCTCACAC</u>

C1

	71						140
H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ10	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
BZ198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGCTGT	CCGCAACGGT
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACGCTGTTGT	TTGCAACGGT
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
Consensus	<u>GCAACCACAC</u>	<u>CAAACGCGCC</u>	<u>TCCGCAACCG</u>	<u>TG--GACCGC</u>	<u>CGTATTGGCG</u>	<u>AC-CTG-TGT</u>	<u>--GCAACGGT</u>

C1

	141						210
H15	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ10	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
BZ198	TCAGGCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
P20	TCAGGCGAAT	GCTACCGATA	CCGAT.....	.GAAGATGAA	GAGTTAGAAT	CCGTAGCACG	CTCTGCTCTG
H38	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAAC	CCGTAGTACG	CTCTGCTCTG
Z2491	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAAT	CCGTACAACG	CTCTGTCTGT
H41	TCAGGCGAAT	GCTACCGATG	AAGAT.....	.GAAGAAGAA	GAGTTAGAAT	CCGTACAACG	CTCTG...TC
EG329	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTGCTACG	CACTGTTGCC
PMC21	TCAGGCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CACTGTTGCC
EG327	TCAGGCGAGT	ACTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
Consensus	<u>TCAGGC-A-T</u>	<u>-CTA-C-AT-</u>	<u>--GA-----</u>	<u>----GA---A</u>	<u>-A-TTAGA--</u>	<u>CCGT---ACG</u>	<u>C-CTG-----</u>

C1

V1

FIG. 2

	211						280
H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ10	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
BZ198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA
Z2491	GGG..AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGCGAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCGAAT	TGGAAACGAT	A.....	TCATTATCAA
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----	-----

V1

	281						350
H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA....	.GTTACCCTC	AAAGCCGGCG	ACAACCTGAA
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
EG327	GAGTATATTT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCCTC	AAAGCCGGCG	ACAACCTGAA
Consensus	-----A---	-----	-----	-----	--T-ACCCTC	AAAGCCGGCG	ACAACCTGAA

V1

C2

	351						420
H15	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ10	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
BZ198	AATCAAACAA	AACACCAATG	AAAACACC..	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA
P20	AATCAAACAA	AGCGGCAAG	A.....CTTCACCTA	CTCGCTGAAA
H38	AATCAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA
Z2491	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
H41	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
EG329	AATCAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA
PMC21	AATCAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA
EG327	AATCAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA
Consensus	AATCAAACAA	A-C-----	-----	-----	-----	-CTTCACCTA	CTC-CTGAAA

C2

V2

C3

FIG. 2

	421						490
H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
P20	AAAGAGCTGA	AAGACCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
Z2491	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
H41	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTGG	CGCAAACAGC	AATAAAGTCA
Consensus	<u>AAAGA-CT-A</u>	<u>-AG--CTGA-</u>	<u>CA-TGTTG-A</u>	<u>ACTGAAAAAT</u>	<u>TATCGTTT-G</u>	<u>CGCAAAC-G-</u>	<u>AA-AAAGTCA</u>

C3

	491						560
H15	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ10	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
BZ198	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
P20	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT
H38	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT
Z2491	ACATCATAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT
H41	ACATCATAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT
EG329	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT
PMC21	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT
EG327	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAAA	AACGGCTGAG	ACCAACGGCG	ACACCACGGT
Consensus	<u>ACATCA-AAG</u>	<u>CGACACCAAA</u>	<u>GGCTTGAATT</u>	<u>T-GCGAAA-A</u>	<u>AACGGCTG-G</u>	<u>AC-AACGGCG</u>	<u>AC-CCACGGT</u>

C3

	561						630
H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG
H38	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATATGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG329	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
PMC21	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC
Consensus	<u>TCATCTGAAC</u>	<u>GGTAT-GGTT</u>	<u>CGACTTTGAC</u>	<u>CGATA-GCT-</u>	<u>--G--T-C--</u>	<u>--GC--C---</u>	<u>----G---C-</u>

C3

V3

FIG.2

631 700

H15	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAAGGA	TGTGTTGAAT	GCGGGTTGGA
H38	AACGACAACG	TTACCGATGA	CAAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAGCAA	GTATTAAAGGA	TGTGTTGAAT	GCGGGTTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGC GGCAA	GCGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	---AC-A--	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA

V3 C4

701 770

H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
P20	ATATTAAGGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	ACACTTACGA
Z2491	ATATTAAGGG	TGTTAAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Consensus	A-ATTAA-GG	-GTTAAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCGTCC	-CACTTACGA

C4 V4 C5

771 840

H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG

C5

841 910

H15	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AAAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTATCA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AAACCGAAG	TTAAAAATCGG	TGCGAAGACT	TCTGTTAT-A	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA

C5

FIG. 2

911 980

H15	AAGGCCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ10	AAGGCCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ198	AAGGCCAAAGA	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
P20	AAGGCCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H38	AAGGCCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Z2491	AAGGCCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H41	AAGGCCAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG329	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
PMC21	AAGACAAAGG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG327	AAGACAAAGG	CGAGAATGAT	TCTTCTACAG	ACAAAGGCCGA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Consensus	<u>AAG-CAAAG-</u>	<u>CGAGAATG-T</u>	<u>TCTTCTACAG</u>	<u>AC-AAAGGCCA</u>	<u>AGGCTTAGTG</u>	<u>ACTGCAAAAG</u>	<u>AAGTGATTGA</u>

C5

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ10	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	<u>TGCAGTAAAC</u>	<u>AAGGCTGGTT</u>	<u>GGAGAATGAA</u>	<u>AACAACAACC</u>	<u>GCTAATGGTC</u>	<u>AAACAGGTCA</u>	<u>AGCTGACAAG</u>

C5

1051 1120

H15	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
BZ10	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
BZ198	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
P20	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
H38	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
Z2491	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
H41	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
EG329	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
PMC21	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
EG327	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACGCG	ACTGTAAGTA
Consensus	<u>TTTGAAACCG</u>	<u>TTACATCAGG</u>	<u>CACAAA-GTA</u>	<u>ACCTTTGCTA</u>	<u>GTGGTAA-GG</u>	<u>TACAACGCG</u>	<u>ACTGTAAGTA</u>

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ10	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	<u>AAGATGATCA</u>	<u>AGGCAACATC</u>	<u>ACTGTTA-GT</u>	<u>ATGATGTAAA</u>	<u>TGTCGGCGAT</u>	<u>GCCCTAAACG</u>	<u>TCAATCAGCT</u>

C5

FIG. 2

	1191		1260
H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ10	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT
Consensus	<u>GCAAAACAGC</u>	<u>GGTTGGAATT</u>	<u>TGGATTCCAA AGCGGTTGCA GGTTCCTTCGG GCAAAGTCAT CAGCGGCAAT</u>

C5

	1261		1330
H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ10	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC
Consensus	<u>GTTTCGCCGA</u>	<u>GCAAGGGAAA</u>	<u>GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC</u>

C5

	1331		1400
H15	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
BZ10	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
BZ198	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
P20	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H38	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Z2491	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
H41	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG329	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
PMC21	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
EG327	GCAACGGCAA	AAATATCGAC	ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG
Consensus	<u>GCAACGG-AA</u>	<u>AAATATCGAC</u>	<u>ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-CGCGG</u>

C5

	1401		1470
H15	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
BZ10	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
BZ198	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TACCAACAAA
P20	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H38	GGCGGATGCG	CCCACTTTGA	GCGTGGATGA CAAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Z2491	GGCAGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
H41	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
EG329	GGCGGATGCG	CCCACTTTGA	GCGTGGAT. . .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
PMC21	GGCGGATGCG	CCCACTTTGA	GCGTGGAT. . .GGGGACGCA TTGAATGTCG GCAGCAAGAA GGACAACAAA
EG327	GGCGGATGCG	CCCACTTTAA	GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA
Consensus	<u>GGC-GATGCG</u>	<u>CCCACTTT-A</u>	<u>GCGTGGAT-- ---GG-CGC- TTGAATGTCG GCAGCAAG-A ---CAACAAA</u>

C5

FIG. 2

1471 1540

H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
B210	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
BZ198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCG	CAACTTAAAG
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCGCA	CAACTTAAAG
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTTAAAGAGG</u>	<u>GGGATGTTAC</u>	<u>AAACGTCGC-</u>	<u>CAACTTAAAG</u>

C5

1541 1610

H15	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TGCCCCAAGC
B210	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TGCCCCAAGC
BZ198	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
P20	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TGCCCCAAGC
H38	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
Z2491	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
H41	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
EG329	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
PMC21	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
EG327	GCGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TGCCCCAAGC
Consensus	<u>G-GTGGCGCA</u>	<u>AAACTTGAAC</u>	<u>AACC-CATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGCG</u>	<u>CG-GCGGG-A</u>	<u>TGCCCCAAGC</u>

C5

1611 1680

H15	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
B210	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
BZ198	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
P20	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
H38	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
Z2491	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
H41	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
EG329	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
PMC21	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
EG327	GATTGCAACC	GCAGGTTTGG	CTCAGGCGTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTA
Consensus	<u>GATTGCAACC</u>	<u>GCAGGT-T-G</u>	<u>-TCAGGC-TA</u>	<u>T-TGCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGGCG--ACT</u>

C5

FIG. 2

FIG. 2

401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgl1del SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD
PMC21 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRLT NVAPGVKEGD
H41Studel TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRLT NVAPGVKEGD
PMC21Bgl1del TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRLT NVAPGVKEGD
PMC21C1C5 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRLT NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPKGSMMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPKGSMMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPKGSMMMA
PMC21Bgl1del VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPKGSMMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPKGSMMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgl1del IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
C5

FIG. 10

1 50

H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVOAS

H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21Bglde1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

C1

51 100

H41 ATDED..EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE

PMC21 ANNEEQEYEL YLHPVQRTVA VLIIVNSDKEG AGEKEKVEEN SDWAVYFNEK

H41Studel ATDE.....

PMC21Bglde1 ANNE.....

PMC21C1C5 AN.....

V1

101 150

H41 FVDPYIVVTI KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK

PMC21 GVLTAAREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK

H41StudelTGLINVETEK

PMC21Bglde1TDLTSVGTEK

PMC21C1C5

V1 C2 V2 C3

151 200

H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21 LSFSAHGKVK NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDTLNT

H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21Bglde1 LSFSAHGKVK NITS DT KGLN FAKETAGTNG DTTVHLNGIG STLTDTLNT

PMC21C1C5

C3 V3

201 250

H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21Bglde1 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21C1C5NVDFVRT

V3 C4 V4 C5

251 300

H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK

H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21Bglde1 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK

PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK

C5

301 350

H41 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

H41Studel KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21Bglde1 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21C1C5 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

C5

351 400

H41 SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21 SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

H41Studel SGTKVTFASG NGTTATVSKD DQGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21Bglde1 SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

PMC21C1C5 SGTNVTFASG KGTTATVSKD DQGNITVMYD VNVGDALNVN QLQNSGWNLD

C5

FIG. 10